

**SPECIFICATION AMENDMENTS**

Please replace the paragraph beginning at page 19, line 17, with the following rewritten paragraph:

The BLAST software suite, freely available sequence comparison algorithms (NCBI, Bethesda MD; <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>), includes various sequence analysis programs including "blastn" that is used to align nucleic acid molecules and BLAST 2 that is used for direct pairwise comparison of either nucleic or amino acid molecules. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity or similarity is measured over the entire length of a sequence or some smaller portion thereof. Brenner *et al.* (1998; Proc Natl Acad Sci 95:6073-6078, incorporated herein by reference) analyzed the BLAST for its ability to identify structural homologs by sequence identity and found 30% identity is a reliable threshold for sequence alignments of at least 150 residues and 40%, for alignments of at least 70 residues.

Please replace the paragraph beginning at page 20, line 23, with the following rewritten paragraph:

Following assembly, templates were subjected to BLAST, motif, and other functional analyses and categorized in protein hierarchies using methods described in USSN 08/812,290 and USSN 08/811,758, both filed March 6, 1997; in USSN 08/947,845, filed October 9, 1997; and in USSN 09/034,807, filed March 4, 1998. Then templates were analyzed by translating each template in all three forward reading frames and searching each translation against the PFAM database of hidden Markov model-based protein families and domains using the HMMER software package (Washington University School of Medicine, St. Louis MO; <http://pfam.wustl.edu/>).

Please amend the Table beginning at p. 22, line 13 as follows:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1 Lipase																				
2 Colipase	11																			
3 Insulin	11	17																		
4 Reg-1 beta	5	5	5																	
5 Reg-1	9	10	12	5																
6 Reg-	7	6	6	7	6															
7 Glucagon	9	11	16	5	10	6														
8 HiAPP	5	4	4	7	4	6	4													
9 2091133	5	4	4	4	2	4	2	6												
10 3836037	5	5	5	4	5	4	5	4	4											
11 3833667	5	5	5	4	5	4	5	4	4	7										
12 3664676	3	5	5	0	5	0	5	0	0	2	2									
13 3835361	5	5	5	2	5	2	5	2	2	4	4	4								
14 884692	3	5	5	2	5	2	5	2	2	2	2	4	4							
15 2383628	14	16	16	5	10	7	12	5	5	5	5	3	5	3						
16 888246	7	6	6	4	4	4	4	4	6	7	7	2	4	2	7					
17 2774542	8	7	7	4	7	6	8	4	4	4	4	2	4	2	9	6				
18 888309	5	5	5	4	5	4	5	4	4	7	7	2	4	2	5	7	4			
19 951335	12	11	11	5	10	7	8	4	4	5	5	3	5	3	13	7	8	5		
20 2777115	11	10	10	3	7	3	7	3	5	6	6	3	6	3	12	8	7	6	10	
21 2075919	11	12	12	5	7	7	7	7	7	5	5	3	5	3	12	7	9	5	13	8